

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gotschlich, Emil C.
- (ii) TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THEM
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Klauber & Jackson
  - (B) STREET: 411 Hackensack Avenue
  - (C) CITY: Hackensack
  - (D) STATE: New Jersey
  - (E) COUNTRY: USA
  - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/312,387
  - (B) FILING DATE: September 26, 1994
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Jackson Esq., David A.
  - (B) REGISTRATION NUMBER: 26,742
  - (C) REFERENCE/DOCKET NUMBER: 600-1-095B
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 201 487-5800
  - (B) TELEFAX: 201 343-1684
  - (C) TELEX: 133521

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5859 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Neisseria gonorrhoeae

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(B) STRAIN: F62

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..381
- (C) GENE: glys (glycyl tRNA synthetase beta chain)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 445..1491
- (C) GENE: lgtA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2342..3262
- (C) GENE: lgtC

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3322..4335
- (C) GENE: lgtD

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4354..5196
- (C) GENE: lgtE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTG CAG GCC GTC GCC GTA TTC AAA CAA CTG CCC GAA GCC GCC GCG CTC	48
Leu Gln Ala Val Ala Val Phe Lys Gln Leu Pro Glu Ala Ala Ala Leu	
1 5 10 15	
GCC GCC GCC AAC AAA CGC GTG CAA AAC CTG CTG AAA AAA GCC GAT GCC	96
Ala Ala Ala Asn Lys Arg Val Gln Asn Leu Leu Lys Lys Ala Asp Ala	
20 25 30	
GCG TTG GGC GAA GTC AAT GAA AGC CTG CTG CAA CAG GAC GAA GAA AAA	144
Ala Leu Gly Glu Val Asn Glu Ser Leu Leu Gln Gln Asp Glu Glu Lys	
35 40 45	
GCC CTG TAC GCT GCC GCG CAA GGT TTG CAG CCG AAA ATT GCC GCC GCC	192
Ala Leu Tyr Ala Ala Ala Gln Gly Leu Gln Pro Lys Ile Ala Ala Ala	
50 55 60	
GTC GCC GAA GGC AAT TTC CGA ACC GCC TTG TCC GAA CTG GCT TCC GTC	240
Val Ala Glu Gly Asn Phe Arg Thr Ala Leu Ser Glu Leu Ala Ser Val	
65 70 75 80	
AAG CCG CAG GTT GAT GCC TTC TTC GAC GGC GTG ATG GTG ATG GCG GAA	288
Lys Pro Gln Val Asp Ala Phe Phe Asp Gly Val Met Val Met Ala Glu	
85 90 95	
GAT GCC GCC GTA AAA CAA AAC CGC CTG AAC CTG CTG AAC CGC TTG GCA	336
Asp Ala Ala Val Lys Gln Asn Arg Leu Asn Leu Leu Asn Arg Leu Ala	
100 105 110	
GAG CAG ATG AAC GCG GTG GCC GAC ATC GCG CTT TTG GGC GAG TAACCGTTGT	388
Glu Gln Met Asn Ala Val Ala Asp Ile Ala Leu Leu Gly Glu	
115 120 125	

ACAGTCCAAA TGCCGTCTGA AGCCTTCAGG CGGCATCAAA TTATCGGGAG AGTAAA	444
TTG CAG CCT TTA GTC AGC GTA TTG ATT TGC GCC TAC AAC GTA GAA AAA Met Gln Pro Leu Val Ser Val Leu Ile Cys Ala Tyr Asn Val Glu Lys 1 5 10 15	492
TAT TTT GCC CAA TCA TTA GCC GCC GTC GTG AAT CAG ACT TGG CGC AAC Tyr Phe Ala Gln Ser Leu Ala Ala Val Val Asn Gln Thr Trp Arg Asn 20 25 30	540
TTG GAT ATT TTG ATT GTC GAT GAC GGC TCG ACA GAC GGC ACA CTT GCC Leu Asp Ile Leu Ile Val Asp Asp Gly Ser Thr Asp Gly Thr Leu Ala 35 40 45	588
ATT GCC AAG GAT TTT CAA AAG CGG GAC AGC CGT ATC AAA ATC CTT GCA Ile Ala Lys Asp Phe Gln Lys Arg Asp Ser Arg Ile Lys Ile Leu Ala 50 55 60	636
CAA GCT CAA AAT TCC GGC CTG ATT CCC TCT TTA AAC ATC GGG CTG GAC Gln Ala Gln Asn Ser Gly Leu Ile Pro Ser Leu Asn Ile Gly Leu Asp 65 70 75 80	684
GAA TTG GCA AAG TCG GGG GGG GGG GGG GAA TAT ATT GCG CGC ACC Glu Leu Ala Lys Ser Gly Gly Gly Gly Glu Tyr Ile Ala Arg Thr 85 90 95	732
GAT GCC GAC GAT ATT GCC TCC CCC GGC TGG ATT GAG AAA ATC GTG GGC Asp Ala Asp Asp Ile Ala Ser Pro Gly Trp Ile Glu Lys Ile Val Gly 100 105 110	780
GAG ATG GAA AAA GAC CGC AGC ATC ATT GCG ATG GGC GCG TGG CTG GAA Glu Met Glu Lys Asp Arg Ser Ile Ile Ala Met Gly Ala Trp Leu Glu 115 120 125	828
GTT TTG TCG GAA GAA AAG GAC GGC AAC CGG CTG GCG CGG CAC CAC AAA Val Leu Ser Glu Glu Lys Asp Gly Asn Arg Leu Ala Arg His His Lys 130 135 140	876
CAC GGC AAA ATT TGG AAA AAG CCG ACC CGG CAC GAA GAC ATC GCC GCC His Gly Lys Ile Trp Lys Lys Pro Thr Arg His Glu Asp Ile Ala Ala 145 150 155 160	924
TTT TTC CCT TTC GGC AAC CCC ATA CAC AAC AAC ACG ATG ATT ATG CGG Phe Phe Pro Phe Gly Asn Pro Ile His Asn Asn Thr Met Ile Met Arg 165 170 175	972
CGC AGC GTC ATT GAC GGC GGT TTG CGT TAC GAC ACC GAG CGG GAT TGG Arg Ser Val Ile Asp Gly Gly Leu Arg Tyr Asp Thr Glu Arg Asp Trp 180 185 190	1020
GCG GAA GAT TAC CAA TTT TGG TAC GAT GTC AGC AAA TTG GGC AGG CTG Ala Glu Asp Tyr Gln Phe Trp Tyr Asp Val Ser Lys Leu Gly Arg Leu 195 200 205	1068
GCT TAT TAT CCC GAA GCC TTG GTC AAA TAC CGC CTT CAC GCC AAT CAG Ala Tyr Tyr Pro Glu Ala Leu Val Lys Tyr Arg Leu His Ala Asn Gln 210 215 220	1116
GTT TCA TCC AAA CAC AGC GTC CGC CAA CAC GAA ATC GCG CAA GGC ATC Val Ser Ser Lys His Ser Val Arg Gln His Glu Ile Ala Gln Gly Ile 225 230 235 240	1164

CAA AAA ACC GCC AGA AAC GAT TTT TTG CAG TCT ATG GGT TTT AAA ACC Gln Lys Thr Ala Arg Asn Asp Phe Leu Gln Ser Met Gly Phe Lys Thr 245 250 255	1212
CGG TTC GAC AGC CTA GAA TAC CGC CAA ACA AAA GCA GCG GCG TAT GAA Arg Phe Asp Ser Leu Glu Tyr Arg Gln Thr Lys Ala Ala Ala Tyr Glu 260 265 270	1260
CTG CCG GAG AAG GAT TTG CCG GAA GAA GAT TTT GAA CGC GCC CGC CGG Leu Pro Glu Lys Asp Leu Pro Glu Glu Asp Phe Glu Arg Ala Arg Arg 275 280 285	1308
TTT TTG TAC CAA TGC TTC AAA CGG ACG GAC ACG CCG CCC TCC GGC GCG Phe Leu Tyr Gln Cys Phe Lys Arg Thr Asp Thr Pro Pro Ser Gly Ala 290 295 300	1356
TGG CTG GAT TTC GCG GCA GAC GGC AGG ATG AGG CGG CTG TTT ACC TTG Trp Leu Asp Phe Ala Ala Asp Gly Arg Met Arg Arg Leu Phe Thr Leu 305 310 315 320	1404
AGG CAA TAC TTC GGC ATT TTG TAC CGG CTG ATT AAA AAC CGC CGG CAG Arg Gln Tyr Phe Gly Ile Leu Tyr Arg Leu Ile Lys Asn Arg Arg Gln 325 330 335	1452
CGC CGG TCG GAT TCG GCA GGG AAA GAA CAG GAG ATT TAATGCAAAA Ala Arg Ser Asp Ser Ala Gly Lys Glu Gln Glu Ile 340 345	1498
CCACGTTATC AGCTTGGCTT CCGCCGCAGA ACGCAGGGCG CACATTGCCG CAACCTTCGG	1558
CAGTCGGCG ATCCCGTTCC AGTTTTCGA CGCACTGATG CCGTCTGAAA GGCTGGAACG	1618
GGCAATGGCG GAACTCGTCC CCGGCTTGTC GGCGCACCCC TATTTGAGCG GAGTGGAAAA	1678
AGCCTGCTTT ATGAGCCACG CCGTATTGTG GGAACAGGCA TTGGACGAAG GCGTACCGTA	1738
TATCGCCGTA TTTGAAGATG ATGTCTTACT CGGCGAAGGC GCGGAGCAGT TCCTTGCCGA	1798
AGATACTTGG CTGCAAGAAC GCTTGACCC CGATTCCGCC TTTGTCGTCC GCTTGGAAAC	1858
GATGTTTATG CACGTCCTGA CCTCGCCCTC CGCGTGGCG GACTACGGCG GGCGGCCCTT	1918
TCCGCTTTG GAAAGCGAAC ACTGCGGGAC GGCGGGCTAT ATTATTCCCC GAAAGGCGAT	1978
GCGTTTTTC TTGGACAGGT TTGCCGTTT GCCGCCGAA CGCCTGCACC CTGTCGATTT	2038
GATGATGTTG GGCAACCCCTG ACGACAGGGA AGGAATGCCG GTTTGCCAGC TCAATCCGC	2098
CTTGTGCGCC CAAGAGCTGC ATTATGCCAA GTTTCACGAC CAAACAGCG CATTGGGCAG	2158
CCTGATCGAA CATGACCGCC GCCTGAACCG CAAACAGCAA TGGCGCGATT CCCCCGCCAA	2218
CACATTCAAA CACCGCCTGA TCCGCGCCTT GACCAAAATC GGCAGGGAAA GGGAAAAACG	2278
CCGGCAAAGG CGCGAACAGT TAATCGGCAA GATTATTGTG CCTTTCCAAT AAAAGGAGAA	2338
AAG ATG GAC ATC GTA TTT GCG GCA GAC GAC AAC TAT GCC GCC TAC CTT Met Asp Ile Val Phe Ala Ala Asp Asp Asn Tyr Ala Ala Tyr Leu 1 5 10 15	2386
TGC GTT GCG GCA AAA AGC GTG GAA GCG GCC CAT CCC GAT ACG GAA ATC Cys Val Ala Ala Lys Ser Val Glu Ala Ala His Pro Asp Thr Glu Ile	2434

	20	25	30	
AGG TTC CAC GTC CTC GAT GCC GGC ATC AGT GAG GAA AAC CGG GCG GCG				2482
Arg Phe His Val Leu Asp Ala Gly Ile Ser Glu Glu Asn Arg Ala Ala	35	40	45	
GTT GCC GCC AAT TTG CGG GGG GGG GGT AAT ATC CGC TTT ATA GAC GTA				2530
Val Ala Ala Asn Leu Arg Gly Gly Asn Ile Arg Phe Ile Asp Val	50	55	60	
AAC CCC GAA GAT TTC GCC GGC TTC CCC TTA AAC ATC AGG CAC ATT TCC				2578
Asn Pro Glu Asp Phe Ala Gly Phe Pro Leu Asn Ile Arg His Ile Ser	65	70	75	
ATT ACG ACT TAT GCC CGC CTG AAA TTG GGC GAA TAC ATT GCC GAT TGC				2626
Ile Thr Thr Tyr Ala Arg Leu Lys Leu Gly Glu Tyr Ile Ala Asp Cys	80	85	90	95
GAC AAA GTC CTG TAT CTG GAT ACG GAC GTA TTG GTC AGG GAC GGC CTG				2674
Asp Lys Val Leu Tyr Leu Asp Thr Asp Val Leu Val Arg Asp Gly Leu	100	105	110	
AAG CCC TTA TGG GAT ACC GAT TTG GGC GGT AAC TGG GTC GGC GCG TGC				2722
Lys Pro Leu Trp Asp Thr Asp Leu Gly Gly Asn Trp Val Gly Ala Cys	115	120	125	
ATC GAT TTG TTT GTC GAA AGG CAG GAA GGA TAC AAA CAA AAA ATC GGT				2770
Ile Asp Leu Phe Val Glu Arg Gln Glu Gly Tyr Lys Gln Lys Ile Gly	130	135	140	
ATG GCG GAC GGA GAA TAT TAT TTC AAT GCC GGC GTA TTG CTG ATC AAC				2818
Met Ala Asp Gly Glu Tyr Tyr Phe Asn Ala Gly Val Leu Leu Ile Asn	145	150	155	
CTG AAA AAG TGG CGG CGG CAC GAT ATT TTC AAA ATG TCC TGC GAA TGG				2866
Leu Lys Lys Trp Arg Arg His Asp Ile Phe Lys Met Ser Cys Glu Trp	160	165	170	175
GTG GAA CAA TAC AAG GAC GTG ATG CAA TAT CAG GAT CAG GAC ATT TTG				2914
Val Glu Gln Tyr Lys Asp Val Met Gln Tyr Gln Asp Gln Asp Ile Leu	180	185	190	
AAC GGG CTG TTT AAA GGC GGG GTG TGT TAT GCG AAC AGC CGT TTC AAC				2962
Asn Gly Leu Phe Lys Gly Val Cys Tyr Ala Asn Ser Arg Phe Asn	195	200	205	
TTT ATG CCG ACC AAT TAT GCC TTT ATG GCG AAC GGG TTT GCG TCC CGC				3010
Phe Met Pro Thr Asn Tyr Ala Phe Met Ala Asn Gly Phe Ala Ser Arg	210	215	220	
CAT ACC GAC CCG CTT TAC CTC GAC CGT ACC AAT ACG GCG ATG CCC GTC				3058
His Thr Asp Pro Leu Tyr Leu Asp Arg Thr Asn Thr Ala Met Pro Val	225	230	235	
GCC GTC AGC CAT TAT TGC GGC TCG GCA AAG CCG TGG CAC AGG GAC TGC				3106
Ala Val Ser His Tyr Cys Gly Ser Ala Lys Pro Trp His Arg Asp Cys	240	245	250	255
ACC GTT TGG GGT GCG GAA CGT TTC ACA GAG TTG GCC GGC AGC CTG ACG				3154
Thr Val Trp Gly Ala Glu Arg Phe Thr Glu Leu Ala Gly Ser Leu Thr	260	265	270	

ACC GTT CCC GAA GAA TGG CGC GGC AAA CTT GCC GTC CCG CCG ACA AAG Thr Val Pro Glu Glu Trp Arg Gly Lys Leu Ala Val Pro Pro Thr Lys 275 280 285	3202
TGT ATG CTT CAA AGA TGG CGC AAA AAG CTG TCT GCC AGA TTC TTA CGC Cys Met Leu Gln Arg Trp Arg Lys Lys Leu Ser Ala Arg Phe Leu Arg 290 295 300	3250
AAG ATT TAT TGACGGGGCA GGCGTCTGA AGCCTTCAGA CGGCATCGGA Lys Ile Tyr 305	3299
CGTATCGGAA AGGAGAAACG GA TTG CAG CCT TTA GTC AGC GTA TTG ATT TGC Met Gln Pro Leu Val Ser Val Leu Ile Cys 1 5 10	3351
GCC TAC AAC GCA GAA AAA TAT TTT GCC CAA TCA TTG GCC GCC GTA GTG Ala Tyr Asn Ala Glu Lys Tyr Phe Ala Gln Ser Leu Ala Ala Val Val 15 20 25	3399
GGG CAG ACT TGG CGC AAC TTG GAT ATT TTG ATT GTC GAT GAC GGC TCG Gly Gln Thr Trp Arg Asn Leu Asp Ile Leu Ile Val Asp Asp Gly Ser 30 35 40	3447
ACG GAC GGC ACG CCC GCC ATT GCC CGG CAT TTC CAA GAA CAG GAC GGC Thr Asp Gly Thr Pro Ala Ile Ala Arg His Phe Gln Glu Gln Asp Gly 45 50 55	3495
AGG ATC AGG ATA ATT TCC AAT CCC CGC AAT TTG GGC TTT ATC GCC TCT Arg Ile Arg Ile Ile Ser Asn Pro Arg Asn Leu Gly Phe Ile Ala Ser 60 65 70	3543
TTA AAC ATC GGG CTG GAC GAA TTG GCA AAG TCG GGG GGG GGG GAA TAT Leu Asn Ile Gly Leu Asp Glu Leu Ala Lys Ser Gly Gly Glu Tyr 75 80 85 90	3591
ATT GCG CGC ACC GAT GCC GAC GAT ATT GCC TCC CCC GGC TGG ATT GAG Ile Ala Arg Thr Asp Ala Asp Asp Ile Ala Ser Pro Gly Trp Ile Glu 95 100 105	3639
AAA ATC GTG GGC GAG ATG GAA AAA GAC CGC AGC ATC ATT GCG ATG GGC Lys Ile Val Gly Glu Met Glu Lys Asp Arg Ser Ile Ile Ala Met Gly 110 115 120	3687
GCG TGG TTG GAA GTT TTG TCG GAA GAA AAC AAT AAA AGC GTG CTT GCC Ala Trp Leu Glu Val Leu Ser Glu Glu Asn Asn Lys Ser Val Leu Ala 125 130 135	3735
GCC ATT GCC CGA AAC GGC GCA ATT TGG GAC AAA CCG ACC CGG CAT GAA Ala Ile Ala Arg Asn Gly Ala Ile Trp Asp Lys Pro Thr Arg His Glu 140 145 150	3783
GAC ATT GTC GCC GTT TTC CCT TTC GGC AAC CCC ATA CAC AAC AAC ACG Asp Ile Val Ala Val Phe Pro Phe Gly Asn Pro Ile His Asn Asn Thr 155 160 165 170	3831
ATG ATT ATG AGG CGC AGC GTC ATT GAC GGC GGT TTG CGG TTC GAT CCA Met Ile Met Arg Arg Ser Val Ile Asp Gly Gly Leu Arg Phe Asp Pro 175 180 185	3879
GCC TAT ATC CAC GCC GAA GAC TAT AAG TTT TGG TAC GAA GCC GGC AAA Ala Tyr Ile His Ala Glu Asp Tyr Lys Phe Trp Tyr Glu Ala Gly Lys	3927

190	195	200	
CTG GGC AGG CTG GCT TAT TAT CCC GAA GCC TTG GTC AAA TAC CGC TTC Leu Gly Arg Leu Ala Tyr Tyr Pro Glu Ala Leu Val Lys Tyr Arg Phe 205	210	215	3975
CAT CAA GAC CAG ACT TCT TCC AAA TAC AAC CTG CAA CAG CGC AGG ACG His Gln Asp Gln Thr Ser Ser Lys Tyr Asn Leu Gln Gln Arg Arg Thr 220	225	230	4023
GCG TGG AAA ATC AAA GAA GAA ATC AGG GCG GGG TAT TGG AAG GCG GCA Ala Trp Lys Ile Lys Glu Glu Ile Arg Ala Gly Tyr Trp Lys Ala Ala 235	240	245	4071
GGC ATA GCC GTC GGG GCG GAC TGC CTG AAT TAC GGG CTT TTG AAA TCA Gly Ile Ala Val Gly Ala Asp Cys Leu Asn Tyr Gly Leu Leu Lys Ser 255	260	265	4119
ACG GCA TAT GCG TTG TAC GAA AAA GCC TTG TCC GGA CAG GAT ATC GGA Thr Ala Tyr Ala Leu Tyr Glu Lys Ala Leu Ser Gly Gln Asp Ile Gly 270	275	280	4167
TGC CTC CGC CTG TTC CTG TAC GAA TAT TTC TTG TCG TTG GAA AAG TAT Cys Leu Arg Leu Phe Leu Tyr Glu Tyr Phe Leu Ser Leu Glu Lys Tyr 285	290	295	4215
TCT TTG ACC GAT TTG CTG GAT TTC TTG ACA GAC CGC GTG ATG AGG AAG Ser Leu Thr Asp Leu Leu Asp Phe Leu Thr Asp Arg Val Met Arg Lys 300	305	310	4263
CTG TTT GCC GCA CCG CAA TAT AGG AAA ATC CTG AAA AAA ATG TTA CGC Leu Phe Ala Ala Pro Gln Tyr Arg Lys Ile Leu Lys Lys Met Leu Arg 315	320	325	4311
CCT TGG AAA TAC CGC AGC TAT TGAAACCGAA CAGGATAAAAT C ATG CAA AAC Pro Trp Lys Tyr Arg Ser Tyr		1	4362
CAC GTT ATC AGC TTG GCT TCC GCC GCA GAG CGC AGG GCG CAC ATT GCC His Val Ile Ser Leu Ala Ser Ala Ala Glu Arg Arg Ala His Ile Ala 5	10	15	4410
GAT ACC TTC GGC AGT CGC GGC ATC CCG TTC CAG TTT TTC GAC GCA CTG Asp Thr Phe Gly Ser Arg Gly Ile Pro Phe Gln Phe Phe Asp Ala Leu 20	25	30	4458
ATG CCG TCT GAA AGG CTG GAA CAG GCG ATG GCG GAA CTC GTC CCC GGC Met Pro Ser Glu Arg Leu Glu Gln Ala Met Ala Glu Leu Val Pro Gly 40	45	50	4506
TTG TCG GCG CAC CCC TAT TTG AGC GGA GTG GAA AAA GCC TGC TTT ATG Leu Ser Ala His Pro Tyr Leu Ser Gly Val Glu Lys Ala Cys Phe Met 55	60	65	4554
AGC CAC GCC GTA TTG TGG GAA CAG GCG TTG GAT GAA GGT CTG CCG TAT Ser His Ala Val Leu Trp Glu Gln Ala Leu Asp Glu Gly Leu Pro Tyr 70	75	80	4602
ATC GCC GTA TTT GAG GAC GAC GTT TTA CTC GGC GAA GGC GCG GAG CAG Ile Ala Val Phe Glu Asp Asp Val Leu Leu Gly Glu Gly Ala Glu Gln 85	90	95	4650

TTC CTT GCC GAA GAT ACT TGG TTG GAA GAG CGT TTT GAC AAG GAT TCC Phe Leu Ala Glu Asp Thr Trp Leu Glu Glu Arg Phe Asp Lys Asp Ser 100 105 110 115	4698
GCC TTT ATC GTC CGT TTG GAA ACG ATG TTT GCG AAA GTT ATT GTC AGA Ala Phe Ile Val Arg Leu Glu Thr Met Phe Ala Lys Val Ile Val Arg 120 125 130	4746
CCG GAT AAA GTC CTG AAT TAT GAA AAC CGG TCA TTT CCT TTG CTG GAG Pro Asp Lys Val Leu Asn Tyr Glu Asn Arg Ser Phe Pro Leu Leu Glu 135 140 145	4794
AGC GAA CAT TGT GGG ACG GCT GGC TAT ATC ATT TCG CGT GAG GCG ATG Ser Glu His Cys Gly Thr Ala Gly Tyr Ile Ile Ser Arg Glu Ala Met 150 155 160	4842
CGG TTT TTC TTG GAC AGG TTT GCC GTT TTG CCG CCA GAG CGG ATT AAA Arg Phe Phe Leu Asp Arg Phe Ala Val Leu Pro Pro Glu Arg Ile Lys 165 170 175	4890
GCG GTA GAT TTG ATG ATG TTT ACT TAT TTC TTT GAT AAG GAG GGG ATG Ala Val Asp Leu Met Met Phe Thr Tyr Phe Phe Asp Lys Glu Gly Met 180 185 190 195	4938
CCT GTT TAT CAG GTT AGT CCC GCC TTA TGT ACC CAA GAA TTG CAT TAT Pro Val Tyr Gln Val Ser Pro Ala Leu Cys Thr Gln Glu Leu His Tyr 200 205 210	4986
GCC AAG TTT CTC AGT CAA AAC AGT ATG TTG GGT AGC GAT TTG GAA AAA Ala Lys Phe Leu Ser Gln Asn Ser Met Leu Gly Ser Asp Leu Glu Lys 215 220 225	5034
GAT AGG GAA CAA GGA AGA AGA CAC CGC CGT TCG TTG AAG GTG ATG TTT Asp Arg Glu Gln Gly Arg Arg His Arg Arg Ser Leu Lys Val Met Phe 230 235 240	5082
GAC TTG AAG CGT GCT TTG GGT AAA TTC GGT AGG GAA AAG AAG AAA AGA Asp Leu Lys Arg Ala Leu Gly Lys Phe Gly Arg Glu Lys Lys Lys Arg 245 250 255	5130
ATG GAG CGT CAA AGG CAG GCG GAG CTT GAG AAA GTT TAC GGC AGG CGG Met Glu Arg Gln Arg Gln Ala Glu Leu Glu Lys Val Tyr Gly Arg Arg 260 265 270 275	5178
GTC ATA TTG TTC AAA TAGTTGTGT AAAATATAGG GGATTAAAAT CAGAAATGGA Val Ile Leu Phe Lys 280	5233
CACACTGTCA TTCCCGCGCA GGCGGAATC TAGGTCTTTA AACTTCGTT TTTCCGATA AATTCTTGCC GCATTAAAAT TCCAGATTCC CGCTTCGCG GGGATGACGG CGGGGGGATT	5293
GTTGCTTTT CGGATAAAAT CCCGTGTTTT TTCATCTGCT AGGTAAAATC GCCCAAAGC GTCTGCATCG CGGCGATGGC GGCGAGTGGG GCGGTTCTG TGCGTAAAAT CCGTTTCCG	5353
AGTGTAAACCG CCTGAAAGCC GGCTCAAAT GCCTGTTGTT CTTCCGTTC TGCCAGCCG CCTTCGGGCC CGACCATAAA GACGATTGCG CCGGACGGGT GGCGGATGTC GCCGAGTTG	5413
CAGGCGCGGT TGATGCTCAT AATCAGCTTG GTGTTTCAG ACGGCATTTC GTCGAGTGCT	5473
	5533
	5593
	5653

TCACGGTAGC CGATGATGGG CAGTACGGGG GGAACGGTGT TCCTGCCGCT TTGTTCGAC	5713
GCGGAGATGA CGATTTCTG CCAGCGTGCAG AGGCCTTGG CGGCGCGTTTC TCCGTCGAGG	5773
CGGACGATGC AGCGTTCGCT GATGACGGGC TGTATGGCGG TTACGCCGAG TTTCGACGCTT	5833
TTTTGCAGGG TGAAATCCAT GCGATC	5859

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu	Gln	Ala	Val	Ala	Val	Phe	Lys	Gln	Leu	Pro	Glu	Ala	Ala	Ala	Leu
1	..	..	..	..	..	5	..	..	..	..	10	..	..	..	15
Ala	Ala	Ala	Asn	Lys	Arg	Val	Gln	Asn	Leu	Leu	Lys	Lys	Ala	Asp	Ala
..	..	..	..	20	..	..	..	..	25	..	..	..	..	30	..
Ala	Leu	Gly	Glu	Val	Asn	Glu	Ser	Leu	Leu	Gln	Gln	Asp	Glu	Glu	Lys
..	..	..	35	..	..	..	40	..	..	..	..	45	..	..	..
Ala	Leu	Tyr	Ala	Ala	Ala	Gln	Gly	Leu	Gln	Pro	Lys	Ile	Ala	Ala	Ala
..	..	..	50	..	..	..	55	..	..	..	..	60	..	..	..
Val	Ala	Glu	Gly	Asn	Phe	Arg	Thr	Ala	Leu	Ser	Glu	Leu	Ala	Ser	Val
..	..	..	65	..	..	70	..	..	..	..	75	..	..	..	80
Lys	Pro	Gln	Val	Asp	Ala	Phe	Phe	Asp	Gly	Val	Met	Val	Met	Ala	Glu
..	..	..	..	85	..	..	..	..	..	90	..	..	..	..	95
Asp	Ala	Ala	Val	Lys	Gln	Asn	Arg	Leu	Asn	Leu	Leu	Asn	Arg	Leu	Ala
..	..	..	100	..	..	..	..	..	105	..	..	..	..	..	110
Glu	Gln	Met	Asn	Ala	Val	Ala	Asp	Ile	Ala	Leu	Leu	Gly	Glu	..	..
..	..	..	115	..	..	..	..	120	..	..	..	..	..	..	125

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Gln	Pro	Leu	Val	Ser	Val	Leu	Ile	Cys	Ala	Tyr	Asn	Val	Glu	Lys
1				5					10					15	
Tyr	Phe	Ala	Gln	Ser	Leu	Ala	Ala	Val	Val	Asn	Gln	Thr	Trp	Arg	Asn
					20				25				30		

Leu Asp Ile Leu Ile Val Asp Asp Gly Ser Thr Asp Gly Thr Leu Ala  
35 40 45

Ile Ala Lys Asp Phe Gln Lys Arg Asp Ser Arg Ile Lys Ile Leu Ala  
50 55 60

Gln Ala Gln Asn Ser Gly Leu Ile Pro Ser Leu Asn Ile Gly Leu Asp  
65 70 75 80

Glu Leu Ala Lys Ser Gly Gly Gly Glu Tyr Ile Ala Arg Thr  
85 90 95

Asp Ala Asp Asp Ile Ala Ser Pro Gly Trp Ile Glu Lys Ile Val Gly  
100 105 110

Glu Met Glu Lys Asp Arg Ser Ile Ile Ala Met Gly Ala Trp Leu Glu  
115 120 125

Val Leu Ser Glu Glu Lys Asp Gly Asn Arg Leu Ala Arg His His Lys  
130 135 140

His Gly Lys Ile Trp Lys Lys Pro Thr Arg His Glu Asp Ile Ala Ala  
145 150 155 160

Phe Phe Pro Phe Gly Asn Pro Ile His Asn Asn Thr Met Ile Met Arg  
165 170 175

Arg Ser Val Ile Asp Gly Gly Leu Arg Tyr Asp Thr Glu Arg Asp Trp  
180 185 190

Ala Glu Asp Tyr Gln Phe Trp Tyr Asp Val Ser Lys Leu Gly Arg Leu  
195 200 205

Ala Tyr Tyr Pro Glu Ala Leu Val Lys Tyr Arg Leu His Ala Asn Gln  
210 215 220

Val Ser Ser Lys His Ser Val Arg Gln His Glu Ile Ala Gln Gly Ile  
225 230 235 240

Gln Lys Thr Ala Arg Asn Asp Phe Leu Gln Ser Met Gly Phe Lys Thr  
245 250 255

Arg Phe Asp Ser Leu Glu Tyr Arg Gln Thr Lys Ala Ala Ala Tyr Glu  
260 265 270

Leu Pro Glu Lys Asp Leu Pro Glu Glu Asp Phe Glu Arg Ala Arg Arg  
275 280 285

Phe Leu Tyr Gln Cys Phe Lys Arg Thr Asp Thr Pro Pro Ser Gly Ala  
290 295 300

Trp Leu Asp Phe Ala Ala Asp Gly Arg Met Arg Arg Leu Phe Thr Leu  
305 310 315 320

Arg Gln Tyr Phe Gly Ile Leu Tyr Arg Leu Ile Lys Asn Arg Arg Gln  
325 330 335

Ala Arg Ser Asp Ser Ala Gly Lys Glu Gln Glu Ile  
340 345

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Ile Val Phe Ala Ala Asp Asp Asn Tyr Ala Ala Tyr Leu Cys  
1 5 10 15

Val Ala Ala Lys Ser Val Glu Ala Ala His Pro Asp Thr Glu Ile Arg  
20 25 30

Phe His Val Leu Asp Ala Gly Ile Ser Glu Glu Asn Arg Ala Ala Val  
35 40 45

Ala Ala Asn Leu Arg Gly Gly Asn Ile Arg Phe Ile Asp Val Asn  
.50 55 60

Pro Glu Asp Phe Ala Gly Phe Pro Leu Asn Ile Arg His Ile Ser Ile  
65 70 75 80

Thr Thr Tyr Ala Arg Leu Lys Leu Gly Glu Tyr Ile Ala Asp Cys Asp  
85 90 95

Lys Val Leu Tyr Leu Asp Thr Asp Val Leu Val Arg Asp Gly Leu Lys  
100 105 110

Pro Leu Trp Asp Thr Asp Leu Gly Gly Asn Trp Val Gly Ala Cys Ile  
115 120 125

Asp Leu Phe Val Glu Arg Gln Glu Gly Tyr Lys Gln Lys Ile Gly Met  
130 135 140

Ala Asp Gly Glu Tyr Tyr Phe Asn Ala Gly Val Leu Leu Ile Asn Leu  
145 150 155 160

Lys Lys Trp Arg Arg His Asp Ile Phe Lys Met Ser Cys Glu Trp Val  
165 170 175

Glu Gln Tyr Lys Asp Val Met Gln Tyr Gln Asp Gln Asp Ile Leu Asn  
180 185 190

Gly Leu Phe Lys Gly Gly Val Cys Tyr Ala Asn Ser Arg Phe Asn Phe  
195 200 205

Met Pro Thr Asn Tyr Ala Phe Met Ala Asn Gly Phe Ala Ser Arg His  
210 215 220

Thr Asp Pro Leu Tyr Leu Asp Arg Thr Asn Thr Ala Met Pro Val Ala  
225 230 235 240

Val Ser His Tyr Cys Gly Ser Ala Lys Pro Trp His Arg Asp Cys Thr  
245 250 255

Val Trp Gly Ala Glu Arg Phe Thr Glu Leu Ala Gly Ser Leu Thr Thr  
260 265 270

Val Pro Glu Glu Trp Arg Gly Lys Leu Ala Val Pro Pro Thr Lys Cys  
275 280 285

Met Leu Gln Arg Trp Arg Lys Lys Leu Ser Ala Arg Phe Leu Arg Lys  
290 295 300

Ile Tyr  
305

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 337 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Gln Pro Leu Val Ser Val Leu Ile Cys Ala Tyr Asn Ala Glu Lys  
1 5 10 15

Tyr Phe Ala Gln Ser Leu Ala Ala Val Val Gly Gln Thr Trp Arg Asn  
20 25 30

Leu Asp Ile Leu Ile Val Asp Asp Gly Ser Thr Asp Gly Thr Pro Ala  
35 40 45

Ile Ala Arg His Phe Gln Glu Gln Asp Gly Arg Ile Arg Ile Ile Ser  
50 55 60

Asn Pro Arg Asn Leu Gly Phe Ile Ala Ser Leu Asn Ile Gly Leu Asp  
65 70 75 80

Glu Leu Ala Lys Ser Gly Gly Glu Tyr Ile Ala Arg Thr Asp Ala  
85 90 95

Asp Asp Ile Ala Ser Pro Gly Trp Ile Glu Lys Ile Val Gly Glu Met  
100 105 110

Glu Lys Asp Arg Ser Ile Ile Ala Met Gly Ala Trp Leu Glu Val Leu  
115 120 125

Ser Glu Glu Asn Asn Lys Ser Val Leu Ala Ala Ile Ala Arg Asn Gly  
130 135 140

Ala Ile Trp Asp Lys Pro Thr Arg His Glu Asp Ile Val Ala Val Phe  
145 150 155 160

Pro Phe Gly Asn Pro Ile His Asn Asn Thr Met Ile Met Arg Arg Ser  
165 170 175

Val Ile Asp Gly Gly Leu Arg Phe Asp Pro Ala Tyr Ile His Ala Glu  
180 185 190

Asp Tyr Lys Phe Trp Tyr Glu Ala Gly Lys Leu Gly Arg Leu Ala Tyr  
195 200 205

Tyr Pro Glu Ala Leu Val Lys Tyr Arg Phe His Gln Asp Gln Thr Ser

210	215	220
Ser Lys Tyr Asn Leu Gln Gln Arg Arg Thr Ala Trp Lys Ile Lys Glu		
225	230	235
Glu Ile Arg Ala Gly Tyr Trp Lys Ala Ala Gly Ile Ala Val Gly Ala		
245	250	255
Asp Cys Leu Asn Tyr Gly Leu Leu Lys Ser Thr Ala Tyr Ala Leu Tyr		
260	265	270
Glu Lys Ala Leu Ser Gly Gln Asp Ile Gly Cys Leu Arg Leu Phe Leu		
275	280	285
Tyr Glu Tyr Phe Leu Ser Leu Glu Lys Tyr Ser Leu Thr Asp Leu Leu		
290	295	300
Asp Phe Leu Thr Asp Arg Val Met Arg Lys Leu Phe Ala Ala Pro Gln		
305	310	315
Tyr Arg Lys Ile Leu Lys Lys Met Leu Arg Pro Trp Lys Tyr Arg Ser		
325	330	335

Tyr

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gln Asn His Val Ile Ser Leu Ala Ser Ala Ala Glu Arg Arg Ala		
1	5	10
His Ile Ala Asp Thr Phe Gly Ser Arg Gly Ile Pro Phe Gln Phe Phe		
20	25	30
Asp Ala Leu Met Pro Ser Glu Arg Leu Glu Gln Ala Met Ala Glu Leu		
35	40	45
Val Pro Gly Leu Ser Ala His Pro Tyr Leu Ser Gly Val Glu Lys Ala		
50	55	60
Cys Phe Met Ser His Ala Val Leu Trp Glu Gln Ala Leu Asp Glu Gly		
65	70	75
Leu Pro Tyr Ile Ala Val Phe Glu Asp Asp Val Leu Leu Gly Glu Gly		
85	90	95
Ala Glu Gln Phe Leu Ala Glu Asp Thr Trp Leu Glu Glu Arg Phe Asp		
100	105	110
Lys Asp Ser Ala Phe Ile Val Arg Leu Glu Thr Met Phe Ala Lys Val		
115	120	125

Ile Val Arg Pro Asp Lys Val Leu Asn Tyr Glu Asn Arg Ser Phe Pro  
130 135 140

Leu Leu Glu Ser Glu His Cys Gly Thr Ala Gly Tyr Ile Ile Ser Arg  
145 150 155 160

Glu Ala Met Arg Phe Phe Leu Asp Arg Phe Ala Val Leu Pro Pro Glu  
165 170 175

Arg Ile Lys Ala Val Asp Leu Met Met Phe Thr Tyr Phe Phe Asp Lys  
180 185 190

Glu Gly Met Pro Val Tyr Gln Val Ser Pro Ala Leu Cys Thr Gln Glu  
195 200 205

Leu His Tyr Ala Lys Phe Leu Ser Gln Asn Ser Met Leu Gly Ser Asp  
210 215 220

Leu Glu Lys Asp Arg Glu Gln Gly Arg Arg His Arg Arg Ser Leu Lys  
225 230 235 240

Val Met Phe Asp Leu Lys Arg Ala Leu Gly Lys Phe Gly Arg Glu Lys  
245 250 255

Lys Lys Arg Met Glu Arg Gln Arg Gln Ala Glu Leu Glu Lys Val Tyr  
260 265 270

Gly Arg Arg Val Ile Leu Phe Lys  
275 280

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5859 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Neisseria gonorrhoeae
  - (B) STRAIN: F62
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1491..2330
  - (C) GENE: lgtB
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGCAGGCCG TCGCCGTATT CAAACAACTG CCCGAAGCCG CCGCGCTCGC CGCCGCCAAC	60
AAACGGGTGC AAAACCTGCT GAAAAAAGCC GATGCCGGT TGGGCGAAGT CAATGAAAGC	120
CTGCTGCAAC AGGACGAAGA AAAAGCCCTG TACGCTGCCG CGCAAGGTTT GCAGCCGAAA	180

ATTGCCGCCG CCGTCGCCGA AGGCAATTTC CGAACCGCCT TGTCCGAAC	240
AAGCCGCAGG TTGATGCCTT CTTCGACGGC GTGATGGTGA TGGCGGAAGA TGCCGCCGTA	300
AAACAAAACC GCCTGAACCT GCTGAACCGC TTGGCAGAGC AGATGAACGC GGTGGCCGAC	360
ATCGCGCTTT TGGGCAGTA ACCGTTGTAC AGTCAAATG CCGTCTGAAG CCTTCAGGCG	420
GCATCAAATT ATCGGGAGAG TAAATTGCAG CCTTTAGTCA GCGTATTGAT TTGCGCCTAC	480
AACGTAGAAA AATATTTGC CCAATCATTA GCCGCCGTCG TGAATCAGAC TTGGCGAAC	540
TTGGATATTT TGATTGTCGA TGACGGCTCG ACAGACGGCA CACTTGCCAT TGCCAAGGAT	600
TTTCAAAAGC GGGACAGCCG TATCAAAATC CTTGCACAAG CTCAAAATTG CGGCCCTGATT	660
CCCTCTTAA ACATCGGGCT GGACGAATTG GCAAAGTCGG GGGGGGGGGG GGGGAATAT	720
ATTGCGCGCA CCGATGCCGA CGATATTGCC TCCCCGGCT GGATTGAGAA AATCGTGGC	780
GAGATGGAAA AAGACCGCAG CATCATTGCG ATGGGCGCGT GGCTGGAAGT TTTGTCGGAA	840
GAAAAGGACG GCAACCGGCT GGCGCGGCA CACAAACACG GCAAATTG GAAAAGCCG	900
ACCCGGCACG AAGACATCGC CGCCTTTTC CCTTCGGCA ACCCCATACA CAACAACACG	960
ATGATTATGC GGCGCAGCGT CATTGACGGC GGTTTGCCTT ACGACACCGA GCGGGATTGG	1020
GCGGAAGATT ACCAATTGTTG GTACGATGTC AGCAAATTGG GCAGGCTGGC TTATTATCCC	1080
GAAGCCTTGG TCAAATACCG CCTTCACGCC AATCAGGTTT CATCCAAACA CAGCGTCCGC	1140
CAACACGAAA TCGCGCAAGG CATCCAAAAA ACCGCCAGAA ACGATTTTT GCAGTCTATG	1200
GGTTTTAAA CCCGGTTCGA CAGCCTAGAA TACCGCCAAA CAAAGCAGC GGCATATGAA	1260
CTGCCGGAGA AGGATTTGCC GGAAGAAGAT TTTGAACGCG CCCGCCGGTT TTTGTACCAA	1320
TGCTTCAAAC GGACGGACAC GCCGCCCTCC GGCGCGTGGC TGGATTCGC GGCAGACGGC	1380
AGGATGAGGC GGCTGTTAC CTTGAGGCAA TACTTCGGCA TTTGTACCG GCTGATTAAA	1440
AACCGCCGGC AGGCGCGGTC GGATTGGCA GGGAAAGAAC AGGAGATTAA ATG CAA	1496
Met Gln	
1	
AAC CAC GTT ATC AGC TTG GCT TCC GCC GCA GAA CGC AGG GCG CAC ATT	1544
Asn His Val Ile Ser Leu Ala Ser Ala Ala Glu Arg Arg Ala His Ile	
5 10 15	
GCC GCA ACC TTC GGC AGT CGC GGC ATC CCG TTC CAG TTT TTC GAC GCA	1592
Ala Ala Thr Phe Gly Ser Arg Gly Ile Pro Phe Gln Phe Phe Asp Ala	
20 25 30	
CTG ATG CCG TCT GAA AGG CTG GAA CGG GCA ATG GCG GAA CTC GTC CCC	1640
Leu Met Pro Ser Glu Arg Leu Glu Arg Ala Met Ala Glu Leu Val Pro	
35 40 45 50	
GGC TTG TCG GCG CAC CCC TAT TTG AGC GGA GTG GAA AAA GCC TGC TTT	1688
Gly Leu Ser Ala His Pro Tyr Leu Ser Gly Val Glu Lys Ala Cys Phe	
55 60 65	

ATG AGC CAC GCC GTA TTG TGG GAA CAG GCA TTG GAC GAA GGC GTA CCG Met Ser His Ala Val Leu Trp Glu Gln Ala Leu Asp Glu Gly Val Pro 70 75 80	1736
TAT ATC GCC GTA TTT GAA GAT GAT GTC TTA CTC GGC GAA GGC GCG GAG Tyr Ile Ala Val Phe Glu Asp Asp Val Leu Leu Gly Glu Gly Ala Glu 85 90 95	1784
CAG TTC CTT GCC GAA GAT ACT TGG CTG CAA GAA CGC TTT GAC CCC GAT Gln Phe Leu Ala Glu Asp Thr Trp Leu Gln Glu Arg Phe Asp Pro Asp 100 105 110	1832
TCC GCC TTT GTC GTC CGC TTG GAA ACG ATG TTT ATG CAC GTC CTG ACC Ser Ala Phe Val Val Arg Leu Glu Thr Met Phe Met His Val Leu Thr 115 120 125 130	1880
TCG CCC TCC GGC GTG GCG GAC TAC GGC GGG CGC GCC TTT CCG CTT TTG Ser Pro Ser Gly Val Ala Asp Tyr Gly Gly Arg Ala Phe Pro Leu Leu 135 140 145	1928
GAA AGC GAA CAC TGC GGG ACG GCG GGC TAT ATT ATT TCC CGA AAG GCG Glu Ser Glu His Cys Gly Thr Ala Gly Tyr Ile Ile Ser Arg Lys Ala 150 155 160	1976
ATG CGT TTT TTC TTG GAC AGG TTT GCC GTT TTG CCG CCC GAA CGC CTG Met Arg Phe Phe Leu Asp Arg Phe Ala Val Leu Pro Pro Glu Arg Leu 165 170 175	2024
CAC CCT GTC GAT TTG ATG ATG TTC GGC AAC CCT GAC GAC AGG GAA GGA His Pro Val Asp Leu Met Met Phe Gly Asn Pro Asp Asp Arg Glu Gly 180 185 190	2072
ATG CCG GTT TGC CAG CTC AAT CCC GCC TTG TGC GCC CAA GAG CTG CAT Met Pro Val Cys Gln Leu Asn Pro Ala Leu Cys Ala Gln Glu Leu His 195 200 205 210	2120
TAT GCC AAG TTT CAC GAC CAA AAC AGC GCA TTG GGC AGC CTG ATC GAA Tyr Ala Lys Phe His Asp Gln Asn Ser Ala Leu Gly Ser Leu Ile Glu 215 220 225	2168
CAT GAC CGC CGC CTG AAC CGC AAA CAG CAA TGG CGC GAT TCC CCC GCC His Asp Arg Arg Leu Asn Arg Lys Gln Gln Trp Arg Asp Ser Pro Ala 230 235 240	2216
AAC ACA TTC AAA CAC CGC CTG ATC CGC GCC TTG ACC AAA ATC GGC AGG Asn Thr Phe Lys His Arg Leu Ile Arg Ala Leu Thr Lys Ile Gly Arg 245 250 255	2264
GAA AGG GAA AAA CGC CGG CAA AGG CGC GAA CAG TTA ATC GGC AAG ATT Glu Arg Glu Lys Arg Arg Gln Arg Arg Glu Gln Leu Ile Gly Lys Ile 260 265 270	2312
ATT GTG CCT TTC CAA TAAAAAGGAGA AAAGATGGAC ATCGTATTG CGGCAGACGA Ile Val Pro Phe Gln 275 280	2367
CAACTATGCC GCCTACCTTT GCGTTGCGGC AAAAAGCGTG GAAGCGGCC ATCCCGATAC GGAAATCAGG TTCCACGTCC TCGATGCCGG CATCAGTGAG GAAAACCGGG CGGGGGTTGC CGCCAATTTG CGGGGGGGGG GTAATATCCG CTTTATAGAC GTAAACCCCG AAGATTCGC	2427 2487 2547

CGGCTTCCCC TTAAACATCA GGCACATTTC CATTACGACT TATGCCGCC TGAAATTGGG	2607
CGAATAACATT GCCGATTGCG ACAAAAGTCCT GTATCTGGAT ACGGACGTAT TGGTCAGGGA	2667
CGGCCTGAAG CCCTTATGGG ATACCGATTT GGGCGGTAAC TGGGTCGGCG CGTGCATCGA	2727
TTTGTGGTC GAAAGGCAGG AAGGATACAA ACAAAAAATC GGTATGGCGG ACGGAGAATA	2787
TTATTTCAAT GCCGGCGTAT TGCTGATCAA CCTGAAAAAG TGGCGGCGC ACGATATTTT	2847
CAAAATGTCC TGCAGATGGG TGGAAACAATA CAAGGACGTG ATGCAATATC AGGATCAGGA	2907
CATTTGAAC GGGCTGTTA AAGGCGGGT GTGTTATGCG AACAGCCGTT TCAACTTTAT	2967
GCCGACCAAT TATGCCCTTA TGGCGAACGG GTTGCGTCC CGCCATACCG ACCCGCTTTA	3027
CCTCGACCGT ACCAATAACGG CGATGCCGT CGCCGTCAGC CATTATTGCG GCTCGGCAA	3087
GCCGTGGCAC AGGGACTGCA CCGTTGGGG TGCGGAACGT TTCACAGAGT TGGCCGGCAG	3147
CCTGACGACC GTTCCCAGG AATGGCGGG CAAACTTGCC GTCCCGCCGA CAAAGTGTAT	3207
GCTTCAAAGA TGGCGAAAAA AGCTGTCG CAGATTCTTA CGCAAGATTT ATTGACGGGG	3267
CAGGCCGTCT GAAGCCTCA GACGGCATCG GACGTATCGG AAAGGAGAAA CGGATTGCAG	3327
CCTTTAGTCA GCGTATTGAT TTGCGCCTAC AACGCAGAAA AATATTTCG CCAATCATTG	3387
GCCGCCGTAG TGGGGCAGAC TTGGCGAAC TTGGATATTT TGATTGTCGA TGACGGCTCG	3447
ACGGACGGCA CGCCCGCCAT TGCCCGCAT TTCCAAGAAC AGGACGGCAG GATCAGGATA	3507
ATTTCCAATC CCCGCAATTG GGGCTTTATC GCCTCTTAA ACATCGGGCT GGACGAATTG	3567
GCAAAGTCGG GGGGGGGGGG ATATATTGCG CGCACCGATG CCGACGATAT TGCCCTCCCC	3627
GGCTGGATTG AGAAAATCGT GGGCGAGATG GAAAAAGACC GCAGCATCAT TGCGATGGGC	3687
GCGTGGTTGG AAGTTTGTC GGAAGAAAAC AATAAAAGCG TGCTTGCCGC CATTGCCCGA	3747
AACGGCGCAA TTTGGGACAA ACCGACCCGG CATGAAGACA TTGTCGCCGT TTTCCCTTTC	3807
GGCAACCCCA TACACAACAA CACGATGATT ATGAGGCGCA GCGTCATTGA CGGCCGTTTG	3867
CGGTTCGATC CAGCCTATAT CCACGCCAA GACTATAAGT TTGGTACGA AGCCGGCAA	3927
CTGGGCAGGC TGGCTTATTA TCCCGAAGCC TTGGTCAAAT ACCGCTTCCA TCAAGACCAG	3987
ACTTCTTCCA AATACAACCT GCAACAGCGC AGGACGGCGT GGAAAATCAA AGAAGAAATC	4047
AGGGCGGGGT ATTGGAAGGC GGCAGGCATA GCCGTCGGGG CGGACTGCCCT GAATTACGGG	4107
CTTTTGAAT CAACGGCATA TGCGTTGTAC GAAAAAGCCT TGTCCGGACA GGATATCGGA	4167
TGCCTCCGCC TGTTCCGTGA CGAATATTTT TTGTCGTTGG AAAAGTATTC TTTGACCGAT	4227
TTGCTGGATT TCTTGACAGA CCGCGTGATG AGGAAGCTGT TTGCCGCACC GCAATATAGG	4287
AAAATCCTGA AAAAAATGTT ACGCCCTTGG AAATACCGCA GCTATTGAAA CGAACAGGA	4347
TAAAATCATGC AAAACCACGT TATCAGCTTG GCTTCCGCCG CAGAGCGCAG GGCGCACATT	4407

GGCGATACCT TCGGCAGTCG CGGCATCCCG TTCCAGTTTT TCGACGCACT GATGCCGTCT	4467
GAAAGGCTGG AACAGGCGAT GGCGGAACTC GTCCCCGGCT TGTCGGCGCA CCCCTATTTG	4527
AGCGGAGTGG AAAAAGCCTG CTTTATGAGC CACGCCGTAT TGTGGGAACA GGCGTTGGAT	4587
GAAGGTCTGC CGTATATCGC CGTATTGAG GACGACGTTT TACTCGGCGA AGGCGCGGAG	4647
CAGTTCTTG CCGAAGATAAC TTGGTTGGAA GAGCGTTTG ACAAGGATTC CGCCTTTATC	4707
TCGCCGTTGG AAACGATGTT TGCGAAAGTT ATTGTCAAGAC CGGATAAAAGT CCTGAATTAT	4767
GAAAACCGGT CATTCCCTT GCTGGAGAGC GAACATTGTG GGACGGCTGG CTATATCATT	4827
TCGCGTGAGG CGATGCGGTT TTTCTTGGAC AGGTTTGCCG TTTTGCCGCC AGAGCGGATT	4887
AAAGCGGTAG ATTGTGATGAT GTTTACTTAT TTCTTTGATA AGGAGGGAT GCCTGTTAT	4947
CAGGTTAGTC CCGCCTTATG TACCCAAGAA TTGCATTATG CCAAGTTCT CAGTCAAAAC	5007
AGTATGTTGG GTAGCGATTT GGAAAAAGAT AGGAAACAAG GAAGAAGACA CCGCCGTTCG	5067
TTGAAGGTGA TGTTTGACTT GAAGCGTGCT TTGGGTAAAT TCGGTAGGGA AAAGAAGAAA	5127
AGAATGGAGC GTCAAAGGCAGCAGCAGCTT GAGAAAGTTT ACGGCAGGCG GGTCAATTG	5187
TTCAAATAGT TTGTGTAAGA TATAGGGAT TAAATCAGA AATGGACACA CTGTCATTCC	5247
CGCGCAGGCG GGAATCTAGG TCTTTAACT TCGGTTTTT CCGATAAATT CTTGCCGCAT	5307
TAAATTCGA GATTCCCGCT TTGCGGGGA TGACGGCGGG GGGATTGTTG CTTTTTCGGA	5367
TAAATCCCG TGTTTTTCA TCTGCTAGGT AAAATCGCCC CAAAGCGTCT GCATCGCGGC	5427
GATGGCGGCG AGTGGGGCGG TTTCTGTGCG TAAATCCGT TTTCCGAGTG TAACCGCCTG	5487
AAAGCCGGCT TCAAATGCCT GTTGTCTTC CTGTTCTGTC CAGCCGCCTT CGGGCCCGAC	5547
CATAAAAGACG ATTGCGCCGG ACGGGTGGCG GATGTCGCCG AGTTTGCAAG CGCGGTTGAT	5607
GCTCATAATC AGCTTGGTGT TTTCAGACGG CATTGTCG AGTGCTTCAC GGTAGCCGAT	5667
GATGGGCAGT ACGGGGGGAA CGGTGTTCCCT GCGCCTTGT TCGCACGCGG AGATGACGAT	5727
TTCCTGCCAG CGTGCAGGGC GTTGGCGGC GCGTTCTCCG TCGAGGCGGA CGATGCAGCG	5787
TTCGCTGATG ACGGGCTGTA TGGCGGTTAC GCGAGTTCG ACGCTTTTT GCAGGGTGAA	5847
ATCCATGCGA TC	5859

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gln Asn His Val Ile Ser Leu Ala Ser Ala Ala Glu Arg Arg Ala  
1 5 10 15

His Ile Ala Ala Thr Phe Gly Ser Arg Gly Ile Pro Phe Gln Phe Phe  
20 25 30

Asp Ala Leu Met Pro Ser Glu Arg Leu Glu Arg Ala Met Ala Glu Leu  
35 40 45

Val Pro Gly Leu Ser Ala His Pro Tyr Leu Ser Gly Val Glu Lys Ala  
50 55 60

Cys Phe Met Ser His Ala Val Leu Trp Glu Gln Ala Leu Asp Glu Gly  
65 70 75 80

Val Pro Tyr Ile Ala Val Phe Glu Asp Asp Val Leu Leu Gly Glu Gly  
85 90 95

Ala Glu Gln Phe Leu Ala Glu Asp Thr Trp Leu Gln Glu Arg Phe Asp  
100 105 110

Pro Asp Ser Ala Phe Val Val Arg Leu Glu Thr Met Phe Met His Val  
115 120 125

Leu Thr Ser Pro Ser Gly Val Ala Asp Tyr Gly Arg Ala Phe Pro  
130 135 140

Leu Leu Glu Ser Glu His Cys Gly Thr Ala Gly Tyr Ile Ile Ser Arg  
145 150 155 160

Lys Ala Met Arg Phe Phe Leu Asp Arg Phe Ala Val Leu Pro Pro Glu  
165 170 175

Arg Leu His Pro Val Asp Leu Met Met Phe Gly Asn Pro Asp Asp Arg  
180 185 190

Glu Gly Met Pro Val Cys Gln Leu Asn Pro Ala Leu Cys Ala Gln Glu  
195 200 205

Leu His Tyr Ala Lys Phe His Asp Gln Asn Ser Ala Leu Gly Ser Leu  
210 215 220

Ile Glu His Asp Arg Arg Leu Asn Arg Lys Gln Gln Trp Arg Asp Ser  
225 230 235 240

Pro Ala Asn Thr Phe Lys His Arg Leu Ile Arg Ala Leu Thr Lys Ile  
245 250 255

Gly Arg Glu Arg Glu Lys Arg Arg Gln Arg Arg Glu Gln Leu Ile Gly  
260 265 270

Lys Ile Ile Val Pro Phe Gln  
275

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCCGAGAAAA CTATTGGTGG A

21

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PCR primer

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAACACATGCA GGAATTGACG AT

22

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 348 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu Gln Pro Leu Val Ser Val Leu Ile Cys Ala Tyr Asn Val Glu Lys  
1 5 10 15

Tyr Phe Ala Gln Ser Leu Ala Ala Val Val Asn Gln Thr Trp Arg Asn  
20 25 30

Leu Asp Ile Leu Ile Val Asp Asp Gly Ser Thr Asp Gly Thr Leu Ala  
35 40 45

Ile Ala Lys Asp Phe Gln Lys Arg Asp Ser Arg Ile Lys Ile Leu Ala  
50 55 60

Gln Ala Gln Asn Ser Gly Leu Ile Pro Ser Leu Asn Ile Gly Leu Asp  
65 70 75 80

Glu Leu Ala Lys Ser Gly Gly Gly Gly Glu Tyr Ile Ala Arg Thr  
85 90 95

Asp Ala Asp Asp Ile Ala Ser Pro Gly Trp Ile Glu Lys Ile Val Gly  
100 105 110

Glu Met Glu Lys Asp Arg Ser Ile Ile Ala Met Gly Ala Trp Leu Glu  
115 120 125

Val Leu Ser Glu Glu Lys Asp Gly Asn Arg Leu Ala Arg His His Lys  
130 135 140

His Gly Lys Ile Trp Lys Lys Pro Thr Arg His Glu Asp Ile Ala Ala  
145 150 155 160

Phe Phe Pro Phe Gly Asn Pro Ile His Asn Asn Thr Met Ile Met Arg  
165 170 175

Arg Ser Val Ile Asp Gly Gly Leu Arg Tyr Asp Thr Glu Arg Asp Trp  
180 185 190

Ala Glu Asp Tyr Gln Phe Trp Tyr Asp Val Ser Lys Leu Gly Arg Leu  
195 200 205

Ala Tyr Tyr Pro Glu Ala Leu Val Lys Tyr Arg Leu His Ala Asn Gln  
210 215 220

Val Ser Ser Lys His Ser Val Arg Gln His Glu Ile Ala Gln Gly Ile  
225 230 235 240

Gln Lys Thr Ala Arg Asn Asp Phe Leu Gln Ser Met Gly Phe Lys Thr  
245 250 255

Arg Phe Asp Ser Leu Glu Tyr Arg Gln Thr Lys Ala Ala Tyr Glu  
260 265 270

Leu Pro Glu Lys Asp Leu Pro Glu Glu Asp Phe Glu Arg Ala Arg Arg  
275 280 285

Phe Leu Tyr Gln Cys Phe Lys Arg Thr Asp Thr Pro Pro Ser Gly Ala  
290 295 300

Trp Leu Asp Phe Ala Ala Asp Gly Arg Met Arg Arg Leu Phe Thr Leu  
305 310 315 320

Arg Gln Tyr Phe Gly Ile Leu Tyr Arg Leu Ile Lys Asn Arg Arg Gln  
325 330 335

Ala Arg Ser Asp Ser Ala Gly Lys Glu Gln Glu Ile  
340 345

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 337 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Gln Pro Leu Val Ser Val Leu Ile Cys Ala Tyr Asn Ala Glu Lys  
1 5 10 15

Tyr Phe Ala Gln Ser Leu Ala Ala Val Val Gly Gln Thr Trp Arg Asn  
20 25 30

Leu Asp Ile Leu Ile Val Asp Asp Gly Ser Thr Asp Gly Thr Pro Ala  
35 40 45

Ile Ala Arg His Phe Gln Glu Gln Asp Gly Arg Ile Arg Ile Ile Ser  
50 55 60

Asn Pro Arg Asn Leu Gly Phe Ile Ala Ser Leu Asn Ile Gly Leu Asp  
65 70 75 80

Glu Leu Ala Lys Ser Gly Gly Glu Tyr Ile Ala Arg Thr Asp Ala  
85 90 95

Asp Asp Ile Ala Ser Pro Gly Trp Ile Glu Lys Ile Val Gly Glu Met  
100 105 110

Glu Lys Asp Arg Ser Ile Ile Ala Met Gly Ala Trp Leu Glu Val Leu  
115 120 125

Ser Glu Glu Asn Asn Lys Ser Val Leu Ala Ala Ile Ala Arg Asn Gly  
130 135 140

Ala Ile Trp Asp Lys Pro Thr Arg His Glu Asp Ile Val Ala Val Phe  
145 150 155 160

Pro Phe Gly Asn Pro Ile His Asn Asn Thr Met Ile Met Arg Arg Ser  
165 170 175

Val Ile Asp Gly Gly Leu Arg Phe Asp Pro Ala Tyr Ile His Ala Glu  
180 185 190

Asp Tyr Lys Phe Trp Tyr Glu Ala Gly Lys Leu Gly Arg Leu Ala Tyr  
195 200 205

Tyr Pro Glu Ala Leu Val Lys Tyr Arg Phe His Gln Asp Gln Thr Ser  
210 215 220

Ser Lys Tyr Asn Leu Gln Gln Arg Arg Thr Ala Trp Lys Ile Lys Glu  
225 230 235 240

Glu Ile Arg Ala Gly Tyr Trp Lys Ala Ala Gly Ile Ala Val Gly Ala  
245 250 255

Asp Cys Leu Asn Tyr Gly Leu Leu Lys Ser Thr Ala Tyr Ala Leu Tyr  
260 265 270

Glu Lys Ala Leu Ser Gly Gln Asp Ile Gly Cys Leu Arg Leu Phe Leu  
275 280 285

Tyr Glu Tyr Phe Leu Ser Leu Glu Lys Tyr Ser Leu Thr Asp Leu Leu  
290 295 300

Asp Phe Leu Thr Asp Arg Val Met Arg Lys Leu Phe Ala Ala Pro Gln  
305 310 315 320

Tyr Arg Lys Ile Leu Lys Lys Met Leu Arg Pro Trp Lys Tyr Arg Ser  
325 330 335

Tyr

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